

**Supplementary Table 1. Whole Exome Sequencing Data Quality Metrics**

<b>Sample</b>	<b>Total Reads</b>	<b>Mean Read Length</b>	<b>Mean Coverage</b>	<b>% Reads Aligned</b>	<b>% Duplicated</b>	<b>% Off Bait</b>	<b>% Usable Bases on Target</b>
II-2	32,711,945	71.9	13.4	98.29	10.94	32.64	36.17
II-4	67,588,605	138.7	64.9	98.87	8.68	7.84	43.98
III-1	38,620,282	72.4	21.5	98.75	15.54	10.69	48.83
III-2	58,760,922	136.3	56.9	98.60	8.03	10.38	45.16
III-4	66,784,500	138.5	65.6	98.82	7.58	7.86	45.06
III-6	14,944,403	72.9	9.3	99.20	10.52	10.71	54.05
III-8	40,723,737	72.6	23.4	98.98	15.53	10.46	50.31
IV-2	34,902,483	73.0	20.4	99.23	15.96	10.67	50.96
IV-4	37,296,478	73.0	21.7	99.30	16.26	10.64	50.60
IV-1	59,281,944	73.0	32.4	99.23	20.34	11.06	47.58